

Figure 1A  
Neutrokin- $\alpha$

1	AAATTCAAGGATAACTCTCTCTGAGGGGTGAGCCCAAGCCCTGCCATGTAGTGCACGCAGGAC	60
61	ATCAACAAACACAGATAACAGGAAATGATCCATTCCTGTGGTCACTTATTCTAAAGGCC	120
121	CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC	180
1	M D D S T E R E Q S R L	12
181	TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTCCATCCTCC	240
13	T S C L K K R E E M K L K E C V S I <u>L P</u>	32
	CD-I	
241	CACGGAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT	300
33	<u>R K E S P S V R S S K D G K L L A A T L</u>	52
	CD-I	
301	TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGCCGCCC	360
53	<u>L L A L L S C C L T V V S F Y Q V A A L</u>	72
361	TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC	420
73	<u>Q G D L A S L R A E L Q G H H A E K L P</u>	92
	CD-II	
421	CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC	480
93	A <u>G A G A P K A G L</u> E E A P A V T A G L	112
	CD-III	
	#	
481	TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA	540
113	K I F E P P A P G E G N S S Q N S R N K	132
541	AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCAAGACTGCTTGCAACTGATTGCAG	600
133	R A V Q G P E E T V T Q D C L <u>Q L I A D</u>	152
	CD-IV	
601	ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT	660
153	S E T P T I Q K G S Y T F <u>V P W L L S F</u>	172
	CD-V	
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT	720
173	<u>K R G S A L E E K E N K I L V K E T G Y</u>	192
	CD-V	
	CD-VI	
721	ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	<u>F F I Y G O V L Y T D K T Y A M G H L I</u>	212
	CD-VI	
	CD-VII	
781	TTCAGAGGAAGAAGGTCCATGTCCTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT	840
213	<u>Q R K K V H V F G D E L S L V T L F R C</u>	232
	CD-VII	
	CD-VIII	
	#	
841	GTATTCAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTACAGCTGGCATTGCAA	900
233	<u>I O N M P E T L P N N S C Y S A G I A K</u>	252
	CD-VIII	
	CD-IX	

[illegible]

901	AACTGGAAGAAGGAGATGAACCTCCAACCTGGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L O L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCCTGTGACCTACTTACACCATGT	1020
273	D G D V <u>T F F G A L K L</u> L	285
	CD-XI	
1021	CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAAA 1100	

FIGURE 2A

	10	20	30	
1	M S T E S M I R D V E L	- - - - -	- - - - - A E E A	TNFalpha
1	M - - - - -	- - - - -	- - - - - T P P E R L	TNFbeta
1	M G A - - - - -	- - - - -	- - - - -	LTbeta
1	M Q Q P F N Y P Y P Q I Y W - V D S S A S S P W A P P G T V			FasLigand
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokin alpha
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokin alphaSV
	40	50	60	
17	L P K K T G G P Q - - G S R R - - - - -			TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - - L G L E G R G G - - - - -			LTbeta
30	L P C P T S V P R R P G Q R R P P P P P P P P L P P P P P			FasLigand
31	L P R K E S P S V R S S K D - - G K L L A A T L L L A L L			Neutrokin alpha
31	L P R K E S P S V R S S K D - - G K L L A A T L L L A L L			Neutrokin alphaSV
	70	80	90	
30	- - - - -	- - - - C L F L S L F S		TNFalpha
9	- - - - - L P R V R G T T L H L L L L G L L L V L L P			TNFbeta
12	- - - - - R L Q G R G S L L L A V A G A T S L V T			LTbeta
60	P P P L P P L P L P P L K K R G N H S T G L C L L V M F F M			FasLigand
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alpha
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alphaSV
	100	110	120	
38	F L - - I V A G A T T L F C L L H F G V I G P Q R E E F P R			TNFalpha
31	G A Q G L P G V G L - - - - -			TNFbeta
32	L L L A V P I T V L A V L A L V P Q D Q G G L V T E T A D P			LTbeta
90	V L V A L V G L G L G M F Q L F H L Q K E L A E L R E S T S			FasLigand
38	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alpha
38	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alphaSV
	130	140	150	
66	D L S L I S - P L A - Q A V R S S S R T P S D - - - K P V A			TNFalpha
41	- - - T P S - A A Q - T A R Q H P K M H L A H S T L K P A A			TNFbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S P G L P A A			LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A			FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T Q D C L			Neutrokin alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T - - - - -			Neutrokin alphaSV
	160	170	180	
91	H V V A N P Q A E G - Q - - - - - L Q W L N R R A N A L L			TNFalpha
66	H L I G D P S K Q N - S - - - - - L L W R A N T D R A F L			TNFbeta
91	H L I G A P L K - G Q G - - - - - L G W E T T K E Q A F L			LTbeta
148	H L T G K S N S R S M P - - - - - L E W E D T Y G I V L L			FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P W L - - - - L S F K			Neutrokin alpha
142	- - - - - - - - - - - G S Y T F V P W L - - - - L S F K			Neutrokin alphaSV

FIGURE 2B

	190	200	210	
114	A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G			TNFalpha
89	Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G			TNFbeta
114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G			LTbeta
172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G			FasLigand
174	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			Neutrokin alpha
155	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			Neutrokin alphaSV
	220	230	240	
143	Q G C P - - - - - S T H V L L T H T I S R I A V S Y Q T K			TNFalpha
118	K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H			TNFbeta
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G			LTbeta
200	Q S C N - - - - - N L P L S H K V Y M R N S K Y P Q D			FasLigand
204	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -			Neutrokin alpha
185	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -			Neutrokin alphaSV
	250	260	270	
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E			TNFalpha
146	V P - - L L S S Q K M V Y P - - - - - G L Q E P W L H			TNFbeta
174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T			LTbeta
222	L V - - M M E G K M M S Y C - - - - - T T G Q M W A R			FasLigand
226	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokin alpha
207	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokin alphaSV
	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E			TNFalpha
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P			TNFbeta
204	S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R			LTbeta
242	S S Y L G A V F N L T S A D H L Y V N V S E L S L V N F E E			FasLigand
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokin alpha
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokin alphaSV
	310			
223	S G Q V Y F G I I A L			TNFalpha
196	S - T V F F G A F A L			TNFbeta
234	- G K T F F G A V M V G			LTbeta
272	S - Q T F F G L Y K L			FasLigand
274	G D V T F F G A L K L L			Neutrokin alpha
255	G D V T F F G A L K L L			Neutrokin alphaSV

Figure 3  
Neutrokinine- $\alpha$

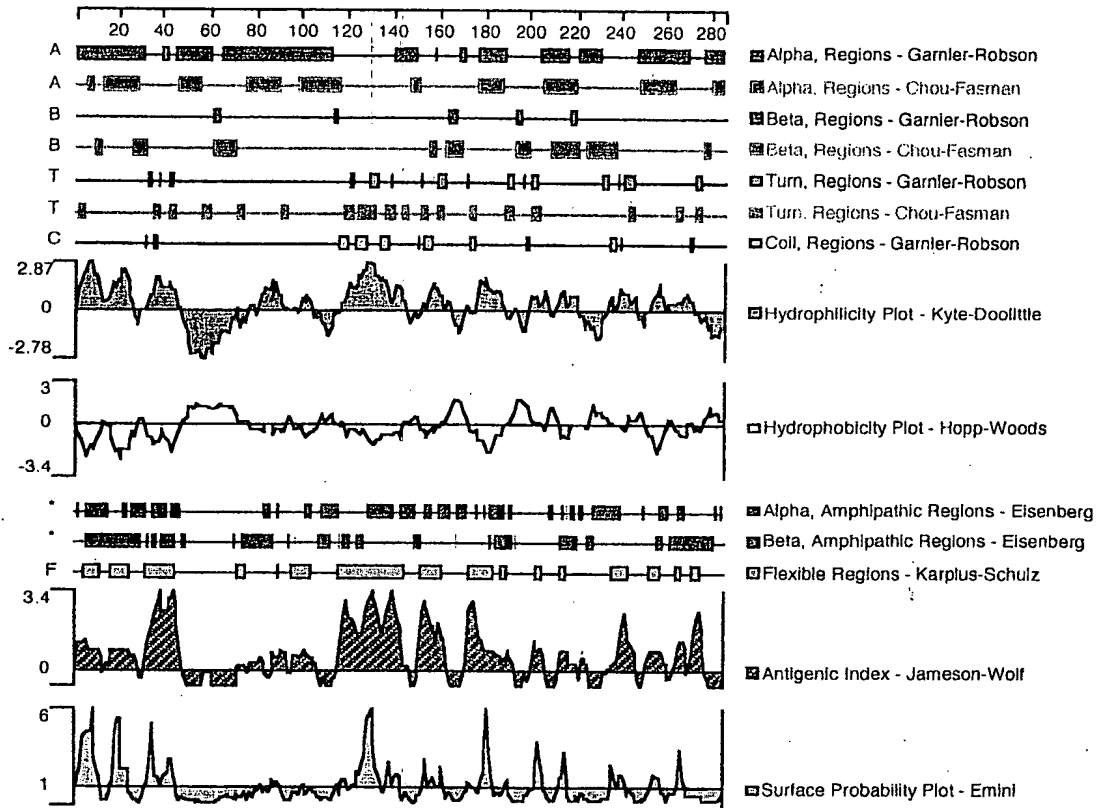


FIGURE 4 A

	1		50
HSOAD55R	.....A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA		
HNEDU15X	...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA		
HSLAH84R	.AATTCGGCA NAGNAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT		
HLTBM08R	AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG		
	51		100
HSOAD55R	GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC		
HNEDU15X	GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC		
HSLAH84R	ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC		
HLTBM08R	GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA		
	101		150
HSOAD55R	CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA		
HNEDU15X	CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA		
HSLAH84R	CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA		
HLTBM08R	GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC		
	151		200
HSOAD55R	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA		
HNEDU15X	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA		
HSLAH84R	AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG		
HLTBM08R	AAGACTGCTT GCAACTGNNT GCAGACAGTG AAACACCAAC TATACAAAAA		
	201		250
HSOAD55R	AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG		
HNEDU15X	AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG		
HSLAH84R	CAAACTGGN AGGAAGGA... ..GATGAAC TCCAACCTGC AATACCAGGG		
HLTBM08R	GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG		
	251		300
HSOAD55R	GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAAG CTGCTGGCTG		
HNEDU15X	GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAAG CTGCTGGCTG		
HSLAH84R	GAAAATGCAC AATTATCACT GGGATGGAGA TGTTACATT TTTTGGGTGC		
HLTBM08R	TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTNCT CTCTGGGAAT		
	301		350
HSOAD55R	CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTNTT.		
HNEDU15X	CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC		
HSLAH84R	CATTGAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC		
HLTBM08R	CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT		
	351		400
HSOAD55R	.....		
HNEDU15X	TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT		
HSLAH84R	CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA		
HLTBM08R	AAGTTTTTAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC		

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FIGURE 4B

	401				450
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC	AGGAGCAGGA	GCCCCCAAGG
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN	GNNANANGNG	GGGNGTTNN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC	AGGTTTNTAT	ANCTGGTAGG
	451				500
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG	CGGGACTGAA	AATCTTTGAA
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN	GGGNNNGTA	AAAATGGGGC
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG	NCNNTCTTTT	GGGNTGA...
	501				550
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT	CAGAACAGCA	GAAATAAGCG
HSLAH84R	CNANGGGGGN	TTTTT.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....
	551				600
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TGCCGTTTCA	GGTCCAGAAG	AAACAGTCAC	TCAAGACTGC	TTGCAACTGA
HSLAH84R	.....	.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....
	601				650
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA	AAGGATCTTA	CACATTTGTT
HSLAH84R	.....	.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....
	651				700
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT	GCCCTAGAAG	AAAAAGAGAA
HSLAH84R	.....	.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....
	701				750
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT	TTTTATATAT	GGTCAGGTTT
HSLAH84R	.....	.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....
	751				800
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC	ATCTAATTCA	GAGGAAGAAG
HSLAH84R	.....	.....	.....	.....	.....
HLTBM08R	.....	.....	.....	.....	.....

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Figure 5A  
Neutrokinine- $\alpha$ SV

1	ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA	60
1	M D D S T E R E Q S R L T S C L K K R E	20
61	GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCCCTCTGTCCGA	120
21	E M K L K E C V S I <u>L P R K E S P S V R</u>	40
	CD-I	
121	TCCTCCAAAGACGGAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC	180
41	<u>S S K D G K L L A A T L L L A L L S C C</u>	60
	CD-I	
181	CTCACGGTGGTGTCTTTTCTACAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG	240
61	<u>L T V V S F Y Q V A A L Q G D L A S L R</u>	80
	CD-II	
241	GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC	300
81	<u>A E L Q G H H A E K L P A G A G A P K A</u>	100
	CD-II	
	CD-III	
301	GGCCTGGAGGAAGCTCCAGCTGTACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA	360
101	<u>G L E E A P A V T A G L K I F E P P A P</u>	120
	CD-III	
	#	
361	GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAGGGTCCAGAAGAA	420
121	G E G N S S Q N S R N K R A V Q G P E E	140
421	ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA	480
141	<u>T G S Y T F V P W L L S F K R G S A L E</u>	160
	CD-IV	
481	GAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATATGGTCAGGTT	540
161	<u>E K E N K I L V K E T G Y F F I Y G Q V</u>	180
	CD-IV	
	CD-V	
541	TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGTCCATGTC	600
181	<u>L Y T D K T Y A M G H L I O R K K V H V</u>	200
	CD-VI	
	CD-VII	
601	TTTGGGGATGAATTGAGTCTGGTGACTTTTGTTCGATGTATTCAAAATATGCCTGAAACA	660
201	<u>F G D E L S L V T L F R C I O N M P E T</u>	220
	CD-VIII	
	#	
661	CTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC	720
221	<u>L P N N S C Y S A G I A K L E E G D E L</u>	240
	CD-IX	
	CD-X	
721	CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT	780
241	<u>Q L A I P R E N A Q I S L D G D V T F F</u>	260
	CD-X	
	CD-XI	
781	GGTGCAATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCTCCCTTTC	840
261	<u>G A L K L L</u>	266
	CD-XI	

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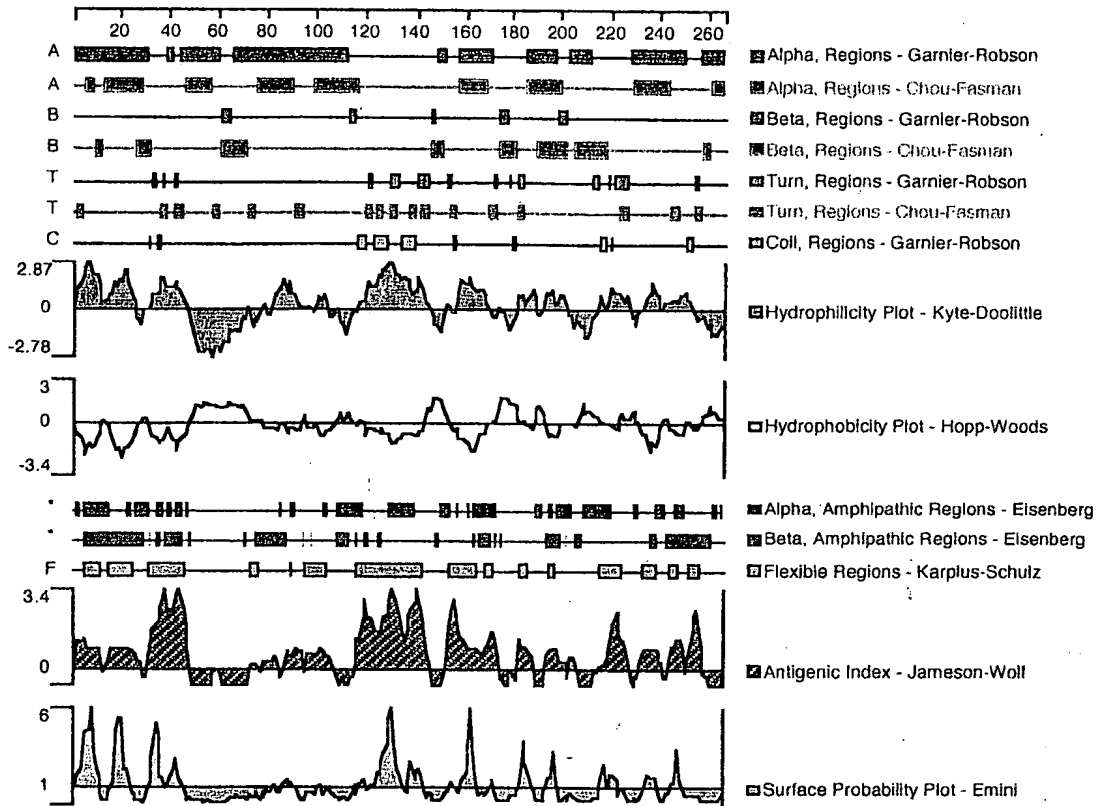
Figure 5B  
Neutrokinine- $\alpha$ SV

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAATACCAAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

[illegible]

Figure 6  
Neutrokinine- $\alpha$ SV



# Figure 7

a.

leutokine-

alpha MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKDGLKLLAATLLALLSCCLTVVSFYQVAALQGDLASLRAE 82

LQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEG 123

NSSQNSRNKRAVQGP EETVT QDC Q L L A E S E P T I Q K G S Y 164  
 April H S V H V P I N A S K - D D S D V 134  
 TNF K P V A H V V N P Q A E G Q - - - - - 102  
 LT α K P A A H L L G D P S K Q N S - - - - - 77

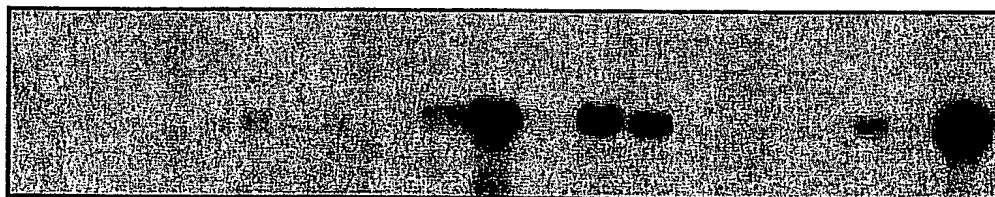
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 E V M W Q P A - - - - F R R G R G I Q A Q G Y G V R I Q D A G V V L L Y S O V L 170  
 - L Q W I N R R A N A L L A N G V E I R D - - N Q I V V P S E G L M L Y S O V L 139  
 - L L W R A N T D R A F Q D G F S E S N - - N S L L V E T S C I Y E V Y S O V V 114

Y T D K L V - - - - A M G S L I Q R K K V H V E G D E L S L V T T F R C L O N M P 237  
 Q D V T F - - - - M G Q V V S R E - - - - G G R Q E T T F R C I R S M P 201  
 K G Q G C P - - - - S T V L E T H T I S R I A V S N Q T K V N L L S A I K S P 176  
 S G A V S P K A T S S P Y T A H E V Q L H S S V P F H V P L L S S O N M V 155

E - - T L E - - - - - N N S C Y S A G I A K L E E G D E F Q L A I P R E N A 268  
 S H P D R A - - - - - N N S C Y S A G V F H H H O G D I F S V I L P R A R A 234  
 C Q R E T P E G A E A K P W Y E P I N L G G V F O L E K G D R L S A E N R P D Y 217  
 Y P - - - - - G L Q E P W L H S M H G A A F O I T O G D Q L E T H T D G I P H 190

Q I S E D G D V D F F G A L K L L 285  
 K L N S E H G H L G F V K L 250  
 D F A E S G Q V Y F G I A E 233  
 V L S - - S T V F L G A F A L 205

b.



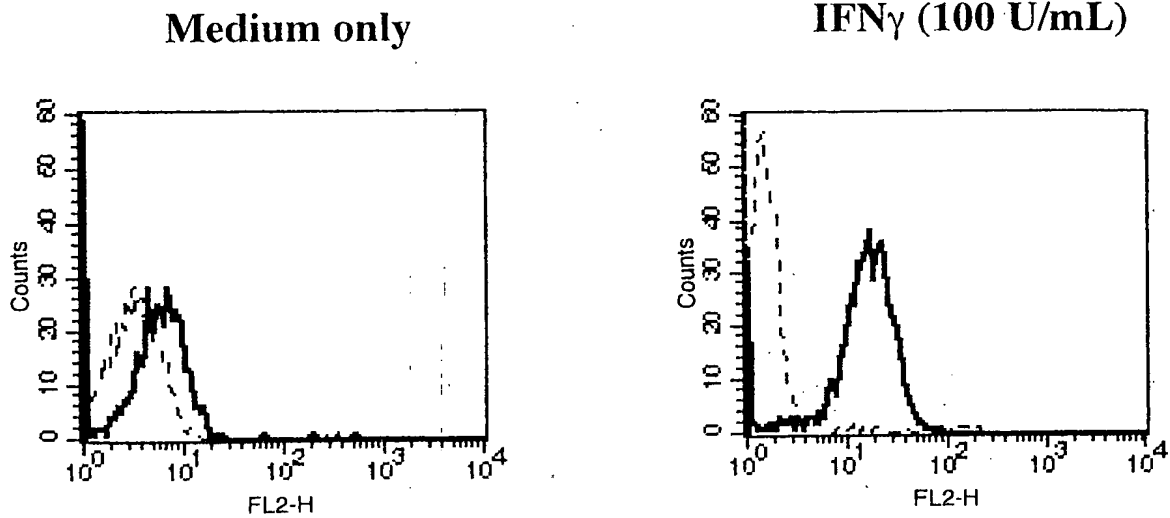
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- 2.4 kb

HL-60  
 HeLa  
 K-562  
 MOLT-4  
 Raji  
 SW480  
 Spleen  
 Lymph Node  
 Thymus  
 PBL  
 Bone Marrow  
 Fetal liver  
 Heart  
 Brain  
 Placenta  
 Lung  
 Liver  
 S. Muscle  
 Kidney  
 Pancreas

Figure 8

a.



b.

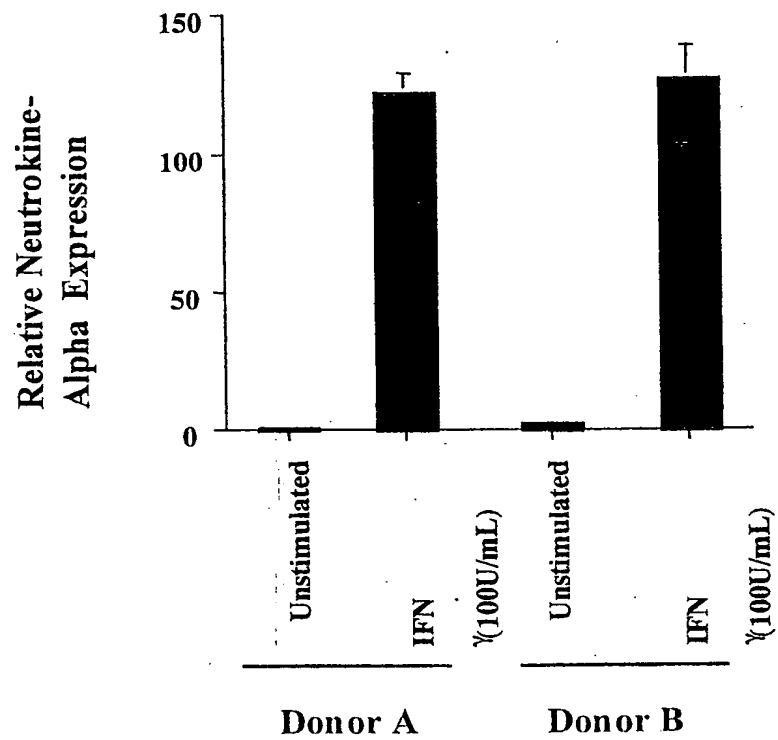
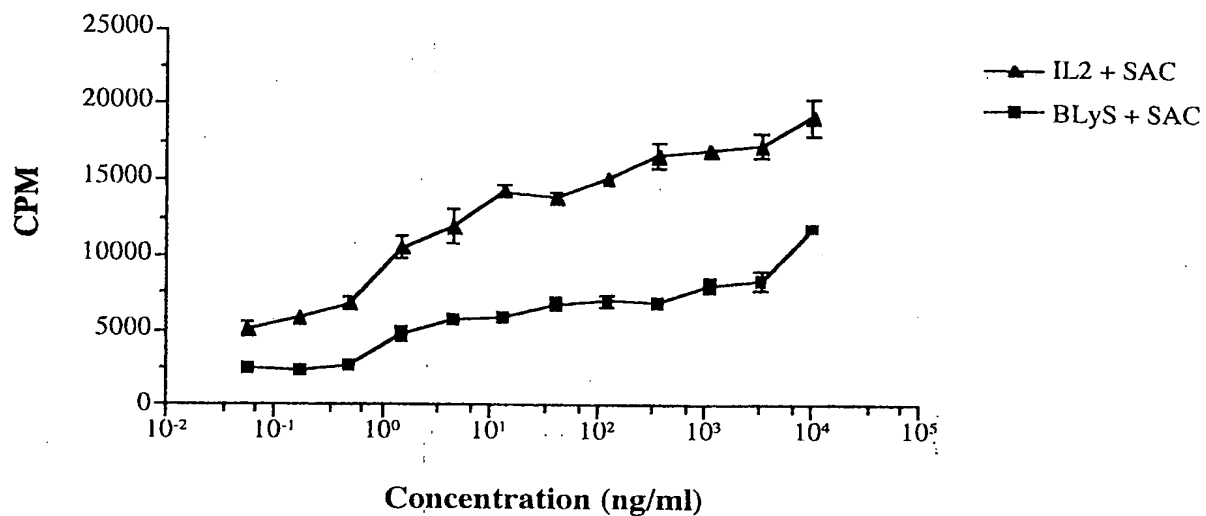
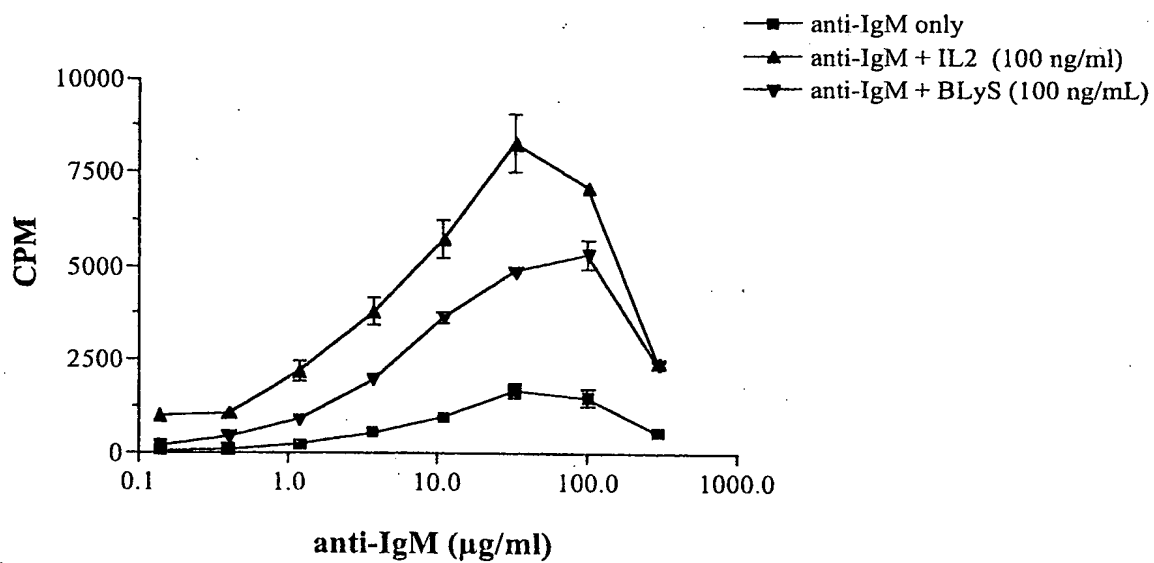


Figure 9

a.



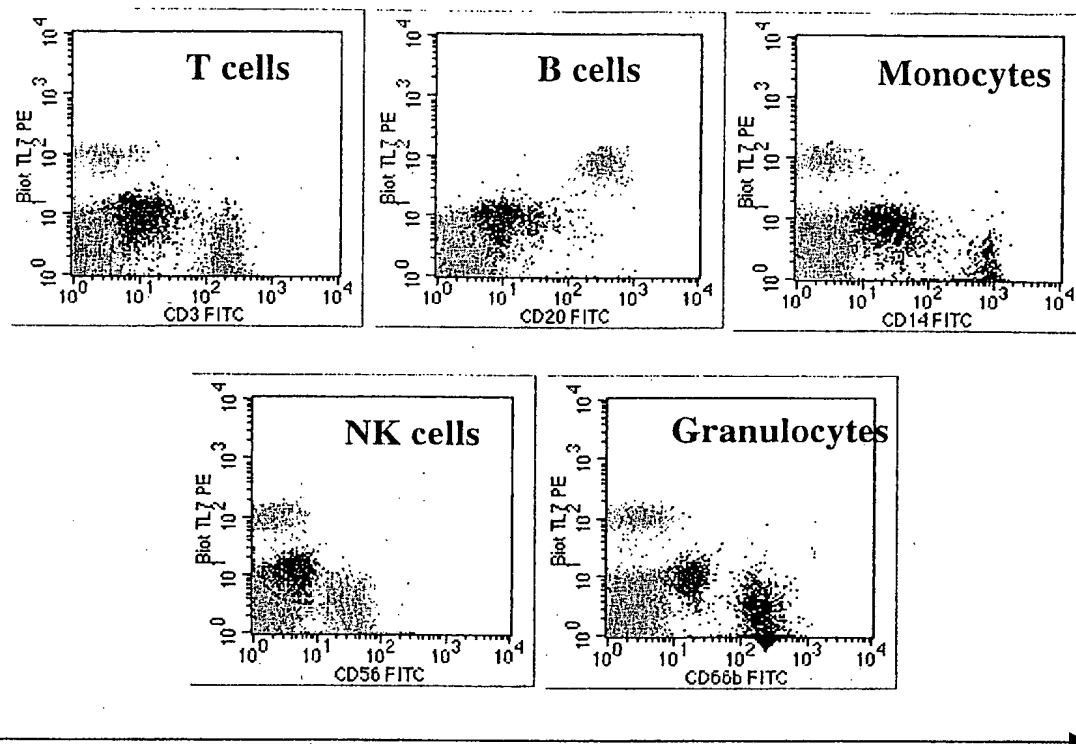
b.



**Figure 10**

**a.**

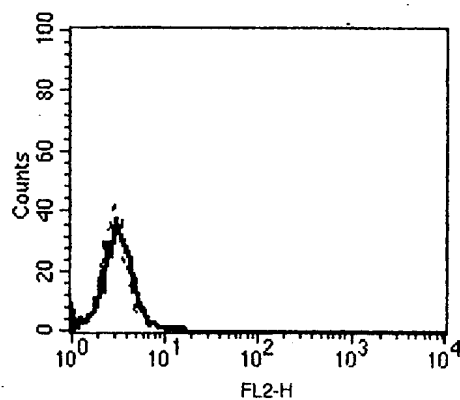
**Biotinylated Neutrokin-  
alpha binding**



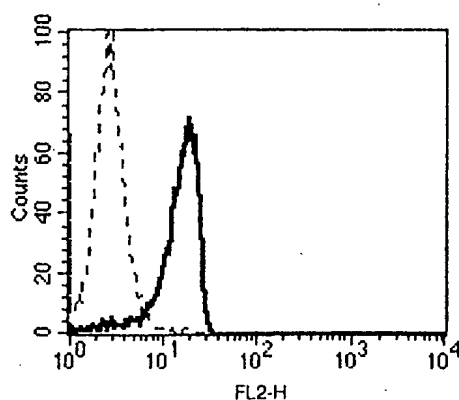
**Hematopoietic lineage markers**

**b.**

**U-937**



**IM-9**



**Figure 11**

